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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 20:51:02 ; Search time 290 Seconds
(without alignments)
8808.124 Million cell updates/sec

Title: US-09-869-079D-2
Perfect score: 1437
Sequence: 1 atgagcgatgtaccattgt.....actctgcaagtgagacagaa 1437

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1437	100.0	1547	3	US-09-851-670-1
2	1354	94.2	1570	3	US-09-526-043-1
3	743	51.7	2410	3	US-09-771-161A-66
4	562	39.1	968	3	US-09-771-161A-65
5	403	28.0	403	3	US-09-474-922A-1
6	285	19.8	387	3	US-09-474-922A-2
7	197	13.7	265	3	US-09-513-999C-2948
8	172	12.0	765	3	US-09-771-161A-64
9	104	7.2	106	3	US-09-513-999C-23043
10	90	6.3	94	3	US-09-513-999C-16008
11	74	5.1	74	3	US-09-526-043-5
12	29	2.0	29	3	US-09-474-922A-3
13	27	1.9	27	3	US-09-474-922A-4
14	27	1.9	27	3	US-09-474-922A-5
15	25	1.7	25	3	US-09-474-922A-6
16	25	1.7	25	3	US-09-474-922A-7
17	25	1.7	25	3	US-09-851-670-6
18	25	1.7	25	3	US-09-851-670-12
19	24	1.7	24	3	US-09-474-922A-8
20	24	1.7	24	3	US-09-851-670-2
21	24	1.7	194	3	US-09-513-999C-35160
22	23	1.6	1254	3	US-09-580-740-3
23	23	1.6	1599	3	US-09-256-465-1
24	23	1.6	1599	3	US-09-167-322-3

25	23	1.6	1599	3	US-09-023-655-1004	Sequence 1004, Ap
26	23	1.6	2181	3	US-09-417-197-70	Sequence 70, Appl
27	23	1.6	2184	3	US-09-417-197-138	Sequence 138, App
28	23	1.6	2239	3	US-09-949-016-1676	Sequence 1676, Ap
29	23	1.6	2599	9	5266464-1	Patent No. 5266464
30	23	1.6	2610	2	US-09-212-771-1	Sequence 1, Appli
31	23	1.6	2610	3	US-09-091-058-1	Sequence 1, Appli
32	23	1.6	2610	3	US-09-023-655-1206	Sequence 1206, Ap
33	23	1.6	2610	3	US-09-590-740-1	Sequence 1, Appli
34	23	1.6	3321	3	US-09-023-655-1361	Sequence 1361, Ap
35	23	1.6	236474	3	US-09-949-016-13418	Sequence 13418, A
36	22	1.5	22	3	US-09-526-043-4	Sequence 4, Appli
37	22	1.5	26	3	US-09-851-670-18	Sequence 18, Appli
38	22	1.5	90	3	US-09-526-043-7	Sequence 7, Appli
39	21	1.5	23	3	US-09-851-670-15	Sequence 15, Appli
40	21	1.5	36	3	US-10-473-785-8	Sequence 8, Appli
41	21	1.5	36	3	US-10-473-763-8	Sequence 8, Appli
42	21	1.5	78491	3	US-09-949-016-15132	Sequence 15132, A
43	20	1.4	25	3	US-09-851-670-19	Sequence 19, Appli
44	20	1.4	48	3	US-10-473-785-10	Sequence 10, Appli
45	20	1.4	48	3	US-10-473-763-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Query Match 100.0%; Score 1437; DB 3; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	71	AAC TGAGGCGCAAGATACCTCTTTTGAAGACAGATGGCTCATTCATAGATATAAGAG	130
Qy	121	AAACCTCAAGATGCGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAG	180
Db	131	AAACCTCAAGATGCGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCAG	190
Qy	181	TTAATGAAACAGAACGACCAACAAAGCCAAACACATTTTATATAGATGTCTCCAGTGGACT	240
Db	251	ACTGTTATAGAGAGAACATTTTCATGTAGATACCTCCAGAGAAAGGAGAAATGGACAGAA	310
Qy	301	GCTATCCAGGCTGTAGCAGACACTGTCAGAGGCAAGAGGAGAGAGAAATGAATTGTAGT	360
Db	311	GCTATCCAGGCTGTAGCAGACACTGTCAGAGGCAAGAGGAGAGAGAAATGAATTGTAGT	370

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QY 371 CCAACTTCACAAATTGATTAATAGGAGAGGAGAGATGGATCCCTCTACAAACCCATCAT 430
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QY 421 AAAAGAAAGACAAATGATTTGACTATTGAAACTACTAGGTAAAGGCACTTTTGGG 480
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QY 431 AAAAGAAAGACAAATGATTTGACTATTGAAACTACTAGGTAAAGGCACTTTTGGG 490
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QY 481 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAG 540
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QY 541 AAAGAAGTCATTTATGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTA 600
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QY 551 AAAGAAGTCATTTATGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTA 610
Db |||||
QY 601 AAGAACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTCCAGACAAAGACCGT 660
Db |||||
QY 611 AAGAACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTCCAGACAAAGACCGT 670
Db |||||
QY 661 TTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCATTTGTGCGAGAGAG 720
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QY 671 TTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCATTTGTGCGAGAGAG 730
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QY 721 CGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGTCAGAAATGTCCTCTGCCCTTGGAC 780
Db |||||
QY 731 CGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGTCAGAAATGTCCTCTGCCCTTGGAC 790
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QY 781 TATCTACATTCGCGAAAGATGTTGTACCGTGATCTCAAGTTGGAGAACTTAATGCTGGAC 840
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QY 841 AAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAGATTTGCAAGAGGGGATCACAGATCA 900
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Db |||||
QY 1151 TTGATAAAGGATCCAAATAAAACGCTTGGTGGAGGACCAAGATGATGCAAAAGAAATTTATG 1210
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QY 1211 AGACACAGTTTCTCTCTGGAATTAACCTGGCAAGATGTATATGATAAAAGCTTGTACCT 1270
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QY 1261 CCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTTGTATGAAGATTTTACA 1320
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QY 1271 CCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTTGTATGAAGATTTTACA 1330
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QY 1321 GCTCAGACTATTACAAATACACCACTGGAATAATATGATGAGGATGGTATGACCTGCGATG 1380
Db |||||
QY 1331 GCTCAGACTATTACAAATACACCACTGGAATAATATGATGAGGATGGTATGACCTGCGATG 1390
Db |||||
QY 1381 GACAAATGAGAGCGGCGCATTTCCCTCAATTTTCTTACTCTGCAAGTGGACGAGAA 1437
Db |||||
QY 1391 GACAAATGAGAGCGGCGCATTTCCCTCAATTTTCTTACTCTGCAAGTGGACGAGAA 1447
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RESULT 2
US-09-526-043-1
; Sequence 1, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
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Query Match          94.2%; Score 1354; DB 3; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  |||||
QY 61  AACTGGAGGCCAAGATACCTTCCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 120
Db  |||||
QY 186 AACTGGAGGCCAAGATACCTTCCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 245
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QY 121 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTTCAGTCGCAAAATGCCAG 180
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QY 246 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTTCAGTCGCAAAATGCCAG 305
Db  |||||
QY 181 TTAATGAAAAACAGAACGACGAAAGCCAAACACATTTTATAATCAGATGTCTCCAGTGGACT 240
Db  |||||
QY 306 TTAATGAAAAACAGAACGACGAAAGCCAAACACATTTTATAATCAGATGTCTCCAGTGGACT 365
Db  |||||
QY 241 ACTGTTATAGAGACACATTTTCATGTAGATACTCCAGAGGAAAGGAAATGGACAGAA 300
Db  |||||
QY 366 ACTGTTATAGAGACACATTTTCATGTAGATACTCCAGAGGAAAGGAAATGGACAGAA 425
Db  |||||
QY 301 GCTATCCAGGCTGTAGCAGACAGACTGCGAGAGGCAAGAGAGGAGAGAAATGAATTTGTAGT 360
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QY 426 GCTATCCAGGCTGTAGCAGACAGACTGCGAGGCGAAGAGGAGAGAGAAATGAATTTGTAGT 485
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QY 361 CCAACTTCACAAATTTGATTAATATAGGAGAGAGAGATGGATGGCTCTACAAACCCATCAT 420
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QY 486 CCAACTTCACAAATTTGATTAATATAGGAGAGAGAGATGGATGGCTCTACAAACCCATCAT 545
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QY 421 AAAAGAAAGACAAATGAATGATTTTGAACCTATTGAAACTACTAGGTAAAGGCACTTTTGGG 480
Db  |||||
QY 546 AAAAGAAAGACAAATGAATGATTTTGAACCTATTGAAACTACTAGGTAAAGGCACTTTTGGG 605
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QY 481 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAAATACTATGCTATCAAGATTTCTGAAG 540
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QY 606 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAAATACTATGCTATGAAGATTTCTGAAG 665
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QY 541 AAAGAAGTCATTTATGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTA 600
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QY 666 AAAGAAGTCATTTATGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTA 725
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QY 601 AAGAACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTCCAGACAAAGACCGT 660
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QY 726 AAGAACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTCCAGACAAAGACCGT 785
Db  |||||
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QY 661 TTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCATTTGTCGAGAGAG 720
Db 786 TTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCATTTGTCGAGAGAG 845
QY 721 CGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATGTCCTCGCTTGGAC 780
Db 846 CGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATGTCCTCGCTTGGAC 905
QY 781 TATCTACATTCGGAAGAATGTTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGAC 840
Db 906 TATCTACATTCGGAAGAATGTTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGAC 965
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Db 1026 GCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGCACACAGAGTGTAGAAATG 1085
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Db 1266 TTGATAAAGGATCCAAATAAACCCCTTGTGTGGAGGACCATGATGCAAAAGAAATTAATG 1325
QY 1201 AGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGATATGATATAAAGCTTTGACCT 1260
Db 1326 AGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGATATGATATAAAGCTTTGACCT 1385
QY 1261 CCTTTAAACCTCAAGTAACTCTGACACAGATAGATATTTGATGAAGATTTTACA 1320
Db 1386 CCTTTAAACCTCAAGTAACTCTGACACAGATAGATATTTGATGAAGATTTTACA 1445
QY 1321 GCTCAGACTATTACAATAACACACACCTGAAAAAT 1354
Db 1446 GCTCAGACTATTACAATAACACACCTGAAAAAT 1479
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RESULT 3

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US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66
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RESULT 4

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US-09-771-161A-65
; Sequence 65, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
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Query Match 51.7%; Score 743; DB 3; Length 2410;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 312 AGCTGTTTTTCCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGCTTTCTATG 371
QY 755 GTGCAAGAAATGTCTGCTGCTTGGACTATCTATACATTCGGAAGAAGATTGTGTACCGTGATC 814
Db 372 GTGCAAGAAATGTCTGCTGCTTGGACTATCTATACATTCGGAAGAAGATTGTGTACCGTGATC 431
QY 815 TCAAGTTCGGAAGATCTAATGCTGGACAAAGATGGCCACATAAAATTAACAGATTTTGGAC 874
Db 432 TCAAGTTCGGAAGATCTAATGCTGGACAAAGATGGCCACATAAAATTAACAGATTTTGGAC 491
QY 875 TTTGCAAAAGAGGGATCACAGATGCAGCCACCATCAAGACATTTCTGTGGCACTCCAGAAAT 934
Db 492 TTTGCAAAAGAGGGATCACAGATGCAGCCACCATCAAGACATTTCTGTGGCACTCCAGAAAT 551
QY 935 ATCTGGCACAGAGGTGTTAGAAATGATCTATGGCCGAGCAGTAGACTGGTGGGGCC 994
Db 552 ATCTGGCACAGAGGTGTTAGAAATGATCTATGGCCGAGCAGTAGACTGGTGGGGCC 611
QY 995 TAGGGGTTGTCATGTATGAATGATGTCTGGGAGGTACCTTTCTACACACAGGACCATG 1054
Db 612 TAGGGGTTGTCATGTATGAATGATGTCTGGGAGGTACCTTTCTACACACAGGACCATG 671
QY 1055 AGAAACTTTTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1114
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QY 1115 ATGCAAAATCATTTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACCGCTTGTGGAG 1174
Db 732 ATGCAAAATCATTTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACCGCTTGTGGAG 791
QY 1175 GACCAGATGATGCAAAAGAAATTAAGACACAGATTTCTCTCGAGTAAACTGGCAAG 1234
Db 792 GACCAGATGATGCAAAAGAAATTAAGACACAGATTTCTCTCGAGTAAACTGGCAAG 851
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QY 1295 CTAGATATTTTGTATGAAGAATTTTACAGCTCAGACTATTACAAATPACCACTCTGAAAAAT 1354
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QY 1355 ATGATGAGGATGTTATGGACTGATGGACATGAGAGGGCGGCATTTCCCTCAATTTT 1414
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QY 1415 CCTACTCTGCAGTGGACGAGAA 1437
Db 1032 CCTACTCTGCAGTGGACGAGAA 1054
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; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(968)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-65

Query Match      39.1%; Score 562; DB 3; Length 968;
Best Local Similarity 100.0%; Pred. No. 4.8e-273;
Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 154 ATGAGCGATGTACCAATTTGAAAGAGGTTGGGTTTCAGAGAGGGGAGAAATATATAAA 213
QY 61 AACTGGAGGCCAAGATACCTCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAG 120
Db 214 AACTGGAGGCCAAGATACCTCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAG 273
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Db 394 ACTGTTATAGAGAGAACATTTTCATGPAGATCTCCAGAGGAAAGGGAAGATGGACAGAA 453
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QY 361 CCAACTTCACAAATTTGATATATAGAGAGGAGAGATGGATGCCCTTACACCCCATCAT 420
Db 514 CCAACTTCACAAATTTGATATATAGAGAGGAGAGATGGATGCCCTTACACCCCATCAT 573
QY 421 AAAAGAGACAAATGAATGATTTTGAAGTACTAGGTAAGGCACTTTTGGG 480
Db 574 AAAAGAGACAAATGAATGATTTTGAAGTACTAGGTAAGGCACTTTTGGG 633
QY 481 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATCTGAAG 540
Db 634 AAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATCTGAAG 693
QY 541 AAAGAGTCATTTATGCAAGG 562
Db 694 AAAGAGTCATTTATGCAAGG 715

RESULT 5
US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowseert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowseert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-474-922A-2
Query Match      19.8%; Score 285; DB 3; Length 387;
Best Local Similarity 99.5%; Pred. No. 2.3e-133;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 962 ATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTTAGGGTTGTTCATGTATGAATGATGT 1021
Db 1 ATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTTAGGGTTGTTCATGTATGAATGATGT 60
QY 1022 GTGGAGGTTACCTTTCTACACCCAGGACCAATGAGAACTTTTGAATTAATTAATG 1081
Db 61 GTGGAGGTTACCTTTCTACACCCAGGACCAATGAGAACTTTTGAATTAATTAATG 120
QY 1082 AAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCT 1141
Db 121 AAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCT 180
QY 1142 TGATAAAGGATCCAAATAAAGCGCTTGTGGAGGACCAAGATGATGCAAAAGAAATTTATGA 1201
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Db 181 TGATAAAGGATCAAAATAAAGCGCTTGGTGGAGGACAGATGACGCAAAAGAAATATGA 240
QY 1202 GACACAGTTTCTCTCTCGAGTAAACTGGCAAGATGTATATGATATAAAAGCTTGTACCTC 1261
Db 241 GACACAGTTTCTCTCTCGAGTAAACTGGCAAGATGTATATGATATAAAAGCTTGTACCTC 300
QY 1262 CTTTAAACCTCAAGTAAACATCTGACACAGACTAGATATTGATGAAGATTTACAG 1321
Db 301 CTCCTAAACCTCAAGTAAACATCTGACACAGACTAGATATTGATGAAGATTTACAG 360
QY 1322 CTCAGACTATTACAATAAACACCACTG 1348
Db 361 CTCAGACTATTACAATAAACCACTG 387

RESULT 7

US-09-513-999C-2948
; Sequence 2948, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2948
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..265
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 116
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 24
; OTHER INFORMATION: Xaa=Leu or Val
US-09-513-999C-2948

Query Match 13.7%; Score 197; DB 3; Length 265;
Best Local Similarity 99.6%; Pred. No. 5.4e-89;
Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 494 TTCAGAGAGGCAAGTGGAAATACTATGCTATGAGATTCTCAAGAAAGAGTCAATTA 553
Db 15 TTCAGAGAGGCAAGTGGAAATACTATGCTATGAGATTCTCAAGAAAGAGTCAATTA 74
QY 554 TTGCAAGAGTGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACACTAGAC 613
Db 75 TTGCAAGAGTGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACACTAGAC 134
QY 614 ATCCCTTTTAAATCCCTTGAATAATTCCTTCCAGACAAAGACCGTTTGTGTTGTGA 673
Db 135 ATCCCTTTTAAATCCCTTGAATAATTCCTTCCAGACAAAGACCGTTTGTGTTGTGA 194
QY 674 TGGATATGTTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGGTGTCTCTG 733
Db 195 TGGATATGTTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGGTGTCTCTG 254

QY 734 AGGACCGC 741
Db 255 AGGACCGC 262

RESULT 8

US-09-771-161A-64
; Sequence 64, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 64
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-64

Query Match 12.0%; Score 172; DB 3; Length 765;
Best Local Similarity 100.0%; Pred. No. 2.3e-76;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCGATGTTACCAATTCGTAAGAGGTTGGGTTTCAGAGAGGGGAGAAATATAAAA 60
Db 154 ATGAGCGATGTTACCAATTCGTAAGAGGTTGGGTTTCAGAGAGGGGAGAAATATAAAA 213
QY 61 AACTGAGGCGCAAGATACCTCTTTGAAGACAGATGGCTCATTCATAGATATAAGAG 120
Db 214 AACTGAGGCGCAAGATACCTCTTTGAAGACAGATGGCTCATTCATAGATATAAGAG 273
QY 121 AACTCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAA 172
Db 274 AACTCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTTCAGTGGCAA 325

RESULT 9

US-09-513-999C-23043
; Sequence 23043, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23043
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23043

Query Match 7.2%; Score 104; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Dec 27 10:45:14 2005

US-09-474-922A-5
 ; Sequence 5, Application US/09474922A
 ; Patent No. 6187586
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowser
 ; APPLICANT: Richard A. Roth
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
 ; FILE REFERENCE: RTS-0036
 ; CURRENT APPLICATION NUMBER: US/09/474,922A
 ; CURRENT FILING DATE: 1999-12-29
 ; NUMBER OF SEQ ID NOS: 89
 ; SEQ ID NO 5
 ; LENGTH: 27
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR Probe
 US-09-474-922A-5

Query Match 1.9%; Score 27; DB 3; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 305 TCAGGCTGTAGCAGACAGACTGCAGA 331
 Db 1 TCCAGGCTGTAGCAGACAGACTGCAGA 27

RESULT 15
 US-09-474-922A-6
 ; Sequence 6, Application US/09474922A
 ; Patent No. 6187586
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowser
 ; APPLICANT: Richard A. Roth
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
 ; FILE REFERENCE: RTS-0036
 ; CURRENT APPLICATION NUMBER: US/09/474,922A
 ; CURRENT FILING DATE: 1999-12-29
 ; NUMBER OF SEQ ID NOS: 89
 ; SEQ ID NO 6
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR Primer
 US-09-474-922A-6

Query Match 1.7%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 GGGCTCTTGATAAAGGATCCAAATA 25

Search completed: December 24, 2005, 00:01:46
 Job time : 292 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2005, 23:51:32 ; Search time 246 Seconds

(without alignments)
3461.187 Million cell updates/sec

Title: US-09-869-079D-3

Perfect score: 479

Sequence: 1 MSDVTIVKEGWQKGEYIK.....MDNRRPHPPQFSYASGRE 479

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Word size: 1

Total number of hits satisfying chosen parameters: 2599977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	479	100.0	1547	3	US-09-851-670-1
2	451	94.2	1570	3	US-09-526-043-1
3	247	51.6	2410	3	US-09-771-161A-66
4	187	39.0	968	3	US-09-771-161A-65
5	134	28.0	403	3	US-09-474-922A-1
6	100	20.9	387	3	US-09-474-922A-2
7	61	12.7	1254	3	US-09-590-740-3
8	61	12.7	2181	3	US-09-417-197-70
9	61	12.7	2184	3	US-09-417-197-138

10	61	12.7	2610	2	US-09-212-771-1	Sequence 1, Appli
11	61	12.7	2610	3	US-09-091-058-1	Sequence 1, Appli
12	61	12.7	2610	3	US-09-023-653-1206	Sequence 1206, Ap
13	61	12.7	2610	3	US-09-590-740-1	Sequence 1, Appli
14	61	12.7	2626	3	US-09-590-740-5	Sequence 5, Appli
15	57	11.9	765	3	US-09-771-161A-64	Sequence 64, Appli
16	52	10.9	1599	3	US-09-256-465-1	Sequence 1, Appli
17	52	10.9	1599	3	US-09-167-322-3	Sequence 1, Appli
18	52	10.9	1599	3	US-09-023-653-1004	Sequence 1004, Ap
19	48	10.0	265	3	US-09-513-999C-2948	Sequence 2948, Ap
20	34	7.1	106	3	US-09-513-999C-23043	Sequence 23043, A
21	29	6.1	94	3	US-09-513-999C-16008	Sequence 16008, A
22	29	5.0	74	3	US-09-526-043-5	Sequence 5, Appli
23	21	4.4	1830	3	US-09-771-161A-41	Sequence 41, Appli
24	15	3.1	532	3	US-09-270-767-14090	Sequence 14090, A
25	14	2.9	1338	3	US-10-067-977-1	Sequence 1, Appli
26	14	2.9	2311	2	US-08-712-709-6	Sequence 6, Appli
27	14	2.9	2311	3	US-09-111-444-6	Sequence 6, Appli
28	14	2.9	2311	3	US-09-541-228-6	Sequence 6, Appli
29	14	2.9	2311	3	US-09-016-434-772	Sequence 772, App
30	14	2.9	2370	3	US-09-031-295-1	Sequence 1, Appli
31	14	2.9	2370	3	US-10-000-039-1	Sequence 1, Appli
32	13	2.7	240	3	US-09-016-434-532	Sequence 532, App
33	12	2.5	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
34	11	2.3	186	3	US-09-270-767-13452	Sequence 13452, A
35	11	2.3	1503	3	US-09-797-039-3	Sequence 3, Appli
36	11	2.3	2297	3	US-09-797-039-1	Sequence 1, Appli
37	11	2.3	2747	3	US-09-620-312D-19	Sequence 19, Appli
38	11	2.3	2840	3	US-09-620-312D-20	Sequence 20, Appli
39	11	2.3	3124	3	US-09-734-030-1	Sequence 1, Appli
40	11	2.3	3124	3	US-10-153-921-1	Sequence 1, Appli
41	11	2.3	3124	3	US-10-669-689-1	Sequence 1, Appli
42	11	2.3	6034	3	US-09-949-016-5830	Sequence 711, App
43	11	2.3	6046	3	US-09-949-016-3586	Sequence 5830, Ap
44	11	2.3	7220	3	US-09-949-016-3586	Sequence 3586, Ap
45	11	2.3	111235	3	US-09-949-016-15328	Sequence 15328, A

ALIGNMENTS

RESULT 1

US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Alignment Scores:
Pred. No.: 0 Length: 1547
Score: 479.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-851-670-1 (1-1547)

Qy 1 MetSerAspValThrIleValLysGluGlyTyrValGlnLysArgGlyGluTyrIleLys 20
Db 11 ATGAGCCATGTTACCATTTGAAAGAGAGTTGGGTTTCAGAGAGGGGAGATATATAAA 70

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QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 71 AACTGAGGCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAGCATATAAAGAG 130
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 131 AAACCTCAAGATGTGGATTTACTCTTATCCCTCAACAACCTTTTCAGTGCCAAATGCCAG 190
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB 191 TTAATGAACAACAGACGACCAAGCCAAACACACATTTATTAATCAGATGCTCCAGTGGACT 250
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpThrGlu 100
DB 251 ACTGTTATAGAGAACATTTCTATGTAGATATCTCCAGAGAAAGGGAATGGACAGAA 310
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
DB 311 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGCGCAAGAGAGAGAGAAATGAATGTAGT 370
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHisHis 140
DB 371 CCAACTTCACAATTTGATTAATAGAGAGAGAGATGCGTCTCTACAAACCCTATCAT 430
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
DB 431 AAAGAAAGACAAATGAATGATTTGACTATTGTAAACTACTAGGTAAGGCACTTTTGGG 490
QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 491 AAAGTTATTTTGGTTCGAGAGAGCGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAG 550
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 551 AAAGAAAGTCATTTATGCAAGGATGAGTGGCACACACTTAACCTGAAAGCAGAGATTATA 610
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 611 AAGAACACCTAGACATCCCTTTTAAACATCCTTGAATAATTTCTTCAGACAAAGACCGT 670
QY 221 LeuCysPheValMetClnTrpValLysGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 671 TTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAG 730
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB 731 CGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTTGCTCTCGCTTGGAC 790
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 791 TATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCTAATGCTGGAC 850
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
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QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 911 GCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTAGAGAT 970
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
DB 971 AATGACTATGGCGGACAGTAGACTGGTGGGCGCTAGGGGTTGTCTATGTATGAATGATG 1030
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB 1031 TGTGGAGGTTTACCTTTCTACAAACAGAGACCATGAGAAACTTTTGAATTAATAATAATG 1090
QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1091 GAAGACATTAATTTCTCGNACACTCTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1150
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DB 1211 AGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATATGATAAAAGCTTGACT 1270
QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1271 CCTTTTAAACCTCAAGTAACATCTGAGACAGACTACTAGATATTTTGTATGAAGAAATTACA 1330
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1331 GCTCAGACTATTACAATAACACCACTGAAAAATATGATGAGGATGGTATGGAATGCGCATG 1390
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1391 GACAATGAGAGCGCGCCGCTTTCCTCAATTTTCTACTCTGCAAGTGGACGAGAA 1447

RESULT 2
US-09-526-043-1
; Sequence 1, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivaachenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
Alignment Scores:
Pred. No.: 0 Length: 1570
Score: 451.00 Matches: 451
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.15% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-526-043-1 (1-1570)
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QY 21 AsnTrpArgProArgTyrPheLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 186 AACTGGAGGCCAAGATATCTCTTTTGAAGACAGATGCTCATTCATAGGATATAAAGAG 245
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 246 AAACCTCAAGATGTGGATTTACCTTTATCCCTTCAACAACTTTTTCAGTGGCAAAATGCCAG 305
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB 306 TTAATGAAAAACAGAACGACCAACCAACACATTTATTAATCAGATGCTCCAGTGGACT 365
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
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Db 366 ACTGTTATAGAGAGAACATTTCTATGATAGATATCTCCAGAGAAAGGAAGATGGACAGAA 425
Qy 101 AlaileGlnAlaValAlaAspArgLeuGlnArgGlnGluArgMetAsnCysSer 120
Db 426 GCTATCCAGCGCTGTAGCAGACAGACTGCAGAGGCAAGAGAGAGAGATGAATTCGTAGT 485
Qy 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrHisHis 140
Db 486 CCAACTTCACAAATTGATAATAGAGAGAGAGATGGATGCCTCTACAACCCATCAT 545
Qy 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluGlyThrPheGly 160
Db 546 AAAAGAAAGCAATGAATGATTTTGACTATTGAACTACTAGTAAAGCACTTTTGGG 605
Qy 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
Db 606 AAAGTTATTTTGGTTCGAGAGAGAGCAAGTGGAAATATCTATCTATGAAGATTCGAAG 665
Qy 181 LysGluValIleLeuLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
Db 666 AAAGAAGTCATTATTGCNAAGGATGAAGTGGCACACACTCTAACTGAAGCAGATATTA 725
Qy 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
Db 726 AAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTTCTTCAGACAAAAGACCGT 785
Qy 221 LeuCysPheValMetGluTyrValAsnGlyGluLeuPhePheHisLeuSerArgGlu 240
Db 786 TTGTGTTTGTGATGGATATGTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGAG 845
Qy 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
Db 846 CGGGTGTCTCTGAGGACCGCACACGTTCTATGTTGCAGAAATTTGCTCTGCTTGGAC 905
Qy 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
Db 906 TATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAGATCTTAATGCTGGAC 965
Qy 281 LysAspGlyHisIleLysIleThrAppPheGlyLeuCysLysGluGlyIleThrAspAla 300
Db 966 AAGATGGCCACATAAAATTTACAGATTTTGGACTTTTGCNAAGAGGGATCACAGATGCA 1025
Qy 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1026 GCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGCCACAGAGGTGTAGAGAT 1085
Qy 321 AsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1086 AATGACTATGCGCAGCAGTAGACTGGTGGGGCTTAGGGTTGTATGTAATGAATG 1145
Qy 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1146 TGTGGGAGGTTTACCTTTCTACAACAGGACCATGAGAACTTTTGAATTAATTAATG 1205
Qy 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
Db 1206 GAAGACATTAATTTCTCGAACACTCTCTCAGATGCAAAATCAITTCITTCAGGGCTC 1265
Qy 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400
Db 1266 TTGNTAAGGATCCAAATTAACCGCTTGTGGAGGACCATGATGCAAAAGAAATATG 1325
Qy 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
Db 1326 AGACACAGTTTCTTCTCTGGAGTAACTGGCAAGATGTATATGATAAAAAGCTTGTACCT 1385
Qy 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db 1386 CCTTTTAAACCTCAAGTAACATCTGAGACAGATATAGATATTTTGTGAAGATTTTACA 1445
Qy 441 AlaGlnThrIleThrIleThrProProGluLys 451
Db 1446 GCTCAGACTATTACAATAACACCCACCTGAAAAA 1478
```

RESULT 3

```
US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66
```

Alignment Scores:

Pred. No.:	1,18e-260	Length:	2410
Score:	247.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	51.57%	Indels:	0
DB:	3	Gaps:	0

US-09-869-079D-3 (1-479) x US-09-771-161A-66 (1-2410)

```
Qy 233 LeuPhePheHisLeuSerArgGluArgValPheSerGluAspArgThrArgPheTyrGly 252
Db 314 CTGTTTTTCCATTTGTCGAGAGAGCGGGTCTCTCTGAGGACCGCACACGCTTTCTATGTT 373
Qy 253 AlaGluIleValSerAlaLeuAspTyrLeuHisSerGlyLysIleValTyrArgAspLeu 272
Db 374 GCAGAAATTTGCTCTCGCTTGGACTATACATTTCCGGAAGATTTGTTACCGGTGATCTC 433
Qy 273 LysLeuGluAsnLeuMetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeu 292
Db 434 AAGTTGGAGAAATCTAATGCTGGCAAGATGGCCACATATAAAATTTACAGATTTTGGACTT 493
Qy 293 CysLysGluGlyIleThrAspAlaIaThrMetLysThrPheCysGlyThrProGluTyr 312
Db 494 TGCAAGAAGGGATCACAGATGCAGCCACCATCAGACATTTCTGTGCACTCCAGAAATAT 553
Qy 313 LeuAlaProGluValLeuGluAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeu 332
Db 554 CTGGCACCGAGGTTGTAGAAATAATGACTATATGGCGGAGCAGTAGACTGGTGGGGCTTA 613
Qy 333 GlyValValMetTyrGluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlu 352
Db 614 GGGTGTGTCATGTATGAATGATGTGTGGAGGTTCCTTTCTACAAACAGGACCATGAG 673
Qy 353 LysLeuPheGluLeuIleLeuMetGluAspIleLysPheProArgThrLeuSerSerAsp 372
Db 674 AAATTTTTGAATTAATTAATTTGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGAT 733
Qy 373 AlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGly 392
Db 734 GCAAAATCATTTGCTTTCAGGGCTCTTCGATAAAGATCCAAATAAACCCCTTTGGTGAGGA 793
Qy 393 ProAspAspAlaLysGluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAsp 412
Db 794 CCAGATGATCAAAAGAAAATTTATGACACACAGATTTCTTCTCTGGAGTAAACTGCAAGAT 853
Qy 413 ValTyrAspLysLysLeuValProPheLysProGlnValThrSerGluThrAspThr 432
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Db      854 GTATATGATAAAAAAGCTTGACTCTCTTTTAAACCTCAAGTAACATCTCTGAGACAGATACT 913
QY      433 ArgTyrPheAspGluGluPheThrAlaGlnThrIleThrIleThrProGluLysTyr 452
Db      914 AGATATTTTGATGAAGAAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAAAATAT 973
QY      453 AspGluAspGlyMetAspCysMetAspAsnGluArgArgProHisPheProGlnPheSer 472
Db      974 GATGAGATGGTATGGACTGCAATGGAACAATGAGAGCGCGCCGATTTCCCTCAATTTTCC 1033
QY      473 TyrSerAlaSerGlyArgGlu 479
Db      1034 TACTCTGCAAGTGGACGAGAA 1054

RESULT 4
US-09-771-161A-65
; Sequence 65, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(968)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-65

Alignment Scores:
Pred. No.:      3,228-195      Length:      968
Score:          187.00      Matches:      187
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     39.04%      Indels:      0
DB:              3          Gaps:          0

US-09-869-079D-3 (1-479) x US-09-771-161A-65 (1-968)

QY      1 MetSerAspValThrIleVallysGluGlyTyrValGlnLysArgGlyGluTyrIleLys 20
Db      154 ATGACCGATGTTTACCATGTGAAAGAGGTTGGGTTCAAGAGGGGAGAAATATATAAA 213
QY      21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
Db      214 AACTGGAGCCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAG 273
QY      41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
Db      274 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTCAGTGCGCAAAATGCCAG 333
QY      61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
Db      334 TTAATGAATAACAGAACCAAGCCAAACACATTTATTAATCAGATGTCCTCAGTGGACT 393
QY      81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
Db      394 ACTGTTATAGAGAGAACATTTTCATGATAGATCTCCAGAGGAAAGGGAAGATGGACAGAA 453
QY      101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
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Db      454 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAGAGAGAGAAATGAATGTAGT 513
QY      121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140
Db      514 CCAACTTCACAAATTTGATAATATAGGAGAGGAAGAGATGGATGCCTCTTACAAACCATCAT 573
QY      141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
Db      574 AAAAGAAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGTAAAGGCACCTTTTGGG 633
QY      161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
Db      634 AAAGTTATTTGGTTTCGAGAGAAAGCAAGTGAAATACTATGCTATGAAGATTTCTGAAG 693
QY      181 LysGluValIleIleAlaLys 187
Db      694 AAAGAAAGTCATTTATGCAAG 714

RESULT 5
US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-1

Alignment Scores:
Pred. No.:      1,89e-137      Length:      403
Score:          134.00      Matches:      134
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     27.97%      Indels:      0
DB:              3          Gaps:          0

US-09-869-079D-3 (1-479) x US-09-474-922A-1 (1-403)

QY      7 VallysGluGlyTyrValGlnLysArgGlyGluTyrIleLysAsnTrpArgProArgTyr 26
Db      1 GTAAAGAAAGGTTGGGTTTCAGAGAGGGGAGAAATATATAAAAACTGCGAGGCCAAGATAC 60
QY      27 PheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGluLysProGlnAspValAsp 46
Db      61 TTCCTTTTGAAGACAGATGGCTCATTCATAGGATATAAAGAGAAACCTCAAGATGTGGAT 120
QY      47 LeuProTyrProLeuAsnAsnPheSerValAlaLysCysGlnLeuMetLysThrGluArg 66
Db      121 TTACCTTATCCCTCAACAACTTTTCAGTGCGCAAAATGCCAGTTAATGAAACAGAACGA 180
QY      67 ProLysProAsnThrPheIleIleArgCysLeuGlnTrpThrThrValIleGluArgThr 86
Db      181 CCAAGGCCAAACACATTTATTAATCAGATGTCTCCAGTGGACTACTGTGTATAGAGAGAA 240
QY      87 PheHisValAspThrProGluGluArgGluGluTrpThrGluAlaIleGlnAlaValAla 106
Db      241 TTTTATGTAGATATCTCCAGAGAAAGGGAAGATGGACAGAGCTATCCAGGCTGTAGCA 300
QY      107 AspArgLeuGlnArgGlnGluGluArgMetAsnCysSerProThrSerGlnIleAsp 126
Db      301 GACAGACTGCAGAGCAAGAGAGAGAGAGATGAATGATTTGTAGTCCACTTCACAAATTTGAT 360
QY      127 AsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140
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Db 361 AATATAGGAGAGAGAGATGGATGCTCTACAAACCATCAT 402

RESULT 6
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2

Alignment Scores:
Pred. No.: 3 66e-100 Length: 387
Score: 100.00 Matches: 127
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 1
Query Match: 20.88% Indels: 2
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-474-922A-2 (1-387)

QY 322 AspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValMetTyrGluMetMetCys 341
Db 3 GACTATGGCCGAGCAGTAGACTGGTGGGCTAGGGCTTGTCTATGATGAATGATGTGT 62
QY 342 GlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMetGlu 361
Db 63 GGAGAGGTACTCTTCTACACACGAGCAGTGGAGAACTTTTGAATTAATTAATGAA 122
QY 362 AspileLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeuLeu 381
Db 123 GACATTAATTTCTCGACACACTCTTCTAGAGCAAAATCATGCTTTTCAGGGCTCTTG 182
QY 382 IleLysAspProAsnLysArgLeuGlyGlyProAspAlaLysGluLeuMetArg 401
Db 183 ATAAAGGATCCAAATAAACGCTTGGTGGAGCAGACGACGCAAAAGAAATTAATGAGA 242
QY 402 HisSerPheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValProPro 421
Db 243 CACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGACCTCT 302
QY 422 Phe-LysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThrAl 441
Db 303 CT-TAAACCTCAAGTAACACTCTGAGCAGACTAGATATTTTGTATGAAGAAATTACAGC 361
QY 441 aGlnThrIleThrIleThrProPro 449
Db 362 TCAGACTATTACATAACACCACT 386

RESULT 7
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Alignment Scores:
Pred. No.: 7 31e-57 Length: 1254
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-590-740-3 (1-1254)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 721 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGCCCCCGAGGTGCTGGAGGAC 780
QY 321 AsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValMetTyrGluMetMet 340
Db 781 AATGACTACGGCGCTGCAGTGGTGGGCGCTGGTCTCATGTACGAGATGATG 840
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
Db 841 TCGGTGCGCTGCCCTTCTACAAACGAGGACCATGAGAAAGCTTTTGAGCTCATCTCATG 900
QY 361 Glu 361
Db 901 GAG 903

RESULT 8
US-09-417-197-70
; Sequence 70, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2178)
US-09-417-197-70

Alignment Scores:
Pred. No.: 1 27e-56 Length: 2181
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-417-197-70 (1-2181)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 910 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGCCCCCGAGGTGCTGGAGGAC 969
QY 321 AsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValMetTyrGluMetMet 340

Db 970 AATGACTACGGCGTGCAGTGCCTGGTGGGGCTGGCGGTGCATGTCATGACGAGATGATG 1029
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1030 TCGGGTGGCTGCCCTTCTACACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1089
QY 361 Glu 361
Db 1090 GAG 1092

RESULT 9

US-09-417-197-138
; Sequence 138, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; FILE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Alignment Scores:

Pred. No.: 1,27e-56 Length: 2184
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-417-197-138 (1-2184)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1651 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1710
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1711 AATGACTACGGCGTGCAGTGCCTGGTGGGGCTGGCGGTGCATGTCATGACGAGATGATG 1770
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1771 TCGGGTGGCTGCCCTTCTACACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1830
QY 361 Glu 361
Db 1831 GAG 1833

RESULT 10

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1

; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Alignment Scores:

Pred. No.: 1,52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 2 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-212-771-1 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1108 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1167
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1168 AATGACTACGGCGTGCAGTGCCTGGTGGGGCTGGCGGTGCATGTCATGACGAGATGATG 1227
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1228 TCGGGTGGCTGCCCTTCTACACACAGGACCATGAGAACCTTTTGAGCTCATCTCATG 1287
QY 361 Glu 361
Db 1288 GAG 1290

RESULT 11

US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Alignment Scores:

Pred. No.: 1,52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-091-058-1 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1108 GCCACATGAAGACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGAC 1167

QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyValValMetTyrGluMetMet 340
DB 1168 AATGACTACGGCGCTGCAGTGGACTGGTGGGGCTGGGCTGTCATGTACGAGATGATG 1227
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
DB 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCTCATG 1287
QY 361 Glu 361
DB 1288 GAG 1290

RESULT 12
US-09-023-655-1206
; Sequence 1206, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G190827
US-09-023-655-1206

Alignment Scores:
Pred. No.: 1.52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-023-655-1206 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320

DB 1108 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCGGAGGTGCTGGAGGAC 1167
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyValValMetTyrGluMetMet 340
DB 1168 AATGACTACGGCGCTGCAGTGGACTGGTGGGGCTGGGCTGTCATGTACGAGATGATG 1227
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
DB 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCTCATG 1287
QY 361 Glu 361
DB 1288 GAG 1290

RESULT 13
US-09-590-740-1
; Sequence 1, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-1

Alignment Scores:
Pred. No.: 1.52e-56 Length: 2610
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0

US-09-869-079D-3 (1-479) x US-09-590-740-1 (1-2610)

QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 1108 GCCACCATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCGGAGGTGCTGGAGGAC 1167
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyValValMetTyrGluMetMet 340
DB 1168 AATGACTACGGCGCTGCAGTGGACTGGTGGGGCTGGGCTGTCATGTACGAGATGATG 1227
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLeuMet 360
DB 1228 TGGGTGCGCTGCCCTTCTACACGAGGACCATGAGAGCTTTTGGAGCTCATCTCATG 1287
QY 361 Glu 361
DB 1288 GAG 1290

RESULT 14
US-09-590-740-5
; Sequence 5, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5
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Alignment Scores:
Pred. No.: 1,53e-56 Length: 2626
Score: 61.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.73% Indels: 0
DB: 3 Gaps: 0
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US-09-869-079D-3 (1-479) x US-09-590-740-5 (1-2626)

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QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db 1193 GCCACTATGAAGACATTCTCGCGAAGCCGCGAGTACTCGGCCCTGAGGTGCTGGAGGAC 1252
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
Db 1253 AACGACTACGGCGGTGACGTGGTGGGGCTGGGGCTGGTGTATGAGATGATG 1312
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db 1313 TGTGGCGCGCTGCCCTTCTACACCGAGACCAGAGAGCTGTTGAGCTGATCCTCATG 1372
QY 361 Glu 361
Db 1373 GAG 1375
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RESULT 15

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US-09-771-161A-64
; Sequence 64, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-64
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Alignment Scores:
Pred. No.: 1,09e-52 Length: 765
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.90% Indels: 0
DB: 3 Gaps: 0
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US-09-869-079D-3 (1-479) x US-09-771-161A-64 (1-765)

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QY 1 MetSerAspValThrIleValLysGluGlyTrpValGlnLysArgGlyGluTyrIleLys 20
Db 154 ATGAGCGATGTTACCATTTGTGAAGAAGCTTGGGTTTCAGAGAGGGGAGATATATATAA 213
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
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Db 214 AACTGGAGGCCAAGATACTTCCCTTTTGAAGACAGATGGCTCATTCATAGATATAAGAG 273
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAla 57
Db 274 AAACCTCAAGATGTGGATTTACCTTTATCCCTCAACAACTTTTCAGTGGCA 324
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Search completed: December 24, 2005, 02:13:53
Job time : 258 secs